



SEQUENCE LISTING

<110> ALBANI, SALVATORE

<120> METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION
AND MODULATION OF ANTIGEN-SPECIFIC T CELLS

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<141> 2003-07-07<150> 09/756,983
<151> 2001-01-09<150> PCT/US99/24666
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<151> 1998-10-20

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived
from third hyper V region of IE molecule of Mus musculus

<400> 1

Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys
1 5 10 15

Ala

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived
from bole I protein of Epstein Barr virus

<400> 2

Thr Arg Asp Asp Ala Glu Tyr Leu Leu Gly Arg Glu Ser Val Leu
1 5 10 15

<210> 3
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide derived from the haemophilus influenza virus

<400> 3
Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys
1 5 10 15

<210> 4
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide derived from the TCR receptor of Mus musculus

<220>
<221> MOD_RES
<222> (18)
<223> Ser, Ile or Thr

<400> 4
Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys
1 5 10 15

Ala Xaa Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro
20 25 30

Gly Thr Arg Leu
35

<210> 5
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide derived from the influenza virus

<400> 5
Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

<210> 6
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide derived from the influenza virus

<400> 6
Val Lys Leu Gly Glu Phe Tyr Asn Gln
1 5

<210> 7
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (2)
<223> cyclohexylalanine

<400> 7
Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala
1 5 10

<210> 8
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide derived from the influenza virus

<400> 8
Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

<210> 9
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 9
Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
1 5 10 15

Arg

<210> 10
<211> 15
<212> PRT
<213> Escherichia coli

<400> 10
Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu
1 5 10 15

<210> 11
<211> 15
<212> PRT
<213> Homo sapiens

<400> 11
Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly
1 5 10 15

<210> 12
<211> 9
<212> PRT
<213> Homo sapiens

<400> 12
Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

<210> 13
<211> 9
<212> PRT
<213> Homo sapiens

<400> 13
Val Lys Leu Gly Glu Phe Tyr Asn Gln
1 5

<210> 14
<211> 13
<212> PRT
<213> Homo sapiens

<400> 14
Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

<210> 15
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct with
 human and bacterial sequences
 <220>
 <221> CDS
 <222> (1)..(939)
 <400> 15
 atg ggc cac aca cgg agg cag gga aca tca cca tcc aag tgt cca tac 48
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1 5 10 15
 ctc aat ttc ttt cag ctc ttg gtg ctg gct ggt ctt tct cac ttc tgt 96
 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 20 25 30
 tca ggt gtt atc cac gtg acc aag gaa gtg aaa gaa gtg gca acg ctg 144
 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 35 40 45
 tcc tgt ggt cac aat gtt tct gtt gaa gag ctg gca caa act cgcc atc 192
 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 50 55 60
 tac tgg caa aag gag aag aaa atg gtg ctg act atg atg tct ggg gac 240
 Tyr Trp Gln Lys Glu Lys Met Val Leu Thr Met Met Ser Gly Asp
 65 70 75 80
 atg aat ata tgg ccc gag tac aag aac cgg acc atc ttt gat atc act 288
 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 85 90 95
 aat aac ctc tcc att gtg atc ctg gct ctg cgc cca tct gac gag ggc 336
 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 100 105 110
 aca tac gag tgt gtt ctg aag tat gaa aaa gac gct ttc aag cgg 384
 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 115 120 125
 gaa cac ctg gct gaa gtg acg tta tca gtc aaa gct gac ttc cct aca 432
 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 130 135 140
 cct agt ata tct gac ttt gaa att cca act tct aat att aga agg ata 480
 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 145 150 155 160
 att tgc tca acc tct gga ggt ttt cca gag cct cac ctc tcc tgg ttg 528
 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 165 170 175
 gaa aat gga gaa gaa tta aat gcc atc aac aca aca gtt tcc caa gat 576
 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
 180 185 190

cct gaa act gag ctc tat gct gtt agc gaa ttc ggc ggc tcc ggt ggt		624	
Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly			
195	200	205	
agc gcc aca cct caa aat att act gat ttg tgt gca gaa tac cac aac		672	
Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn			
210	215	220	
aca caa ata cat acg cta aat gat aag ata ttt tcg tat aca gaa tct		720	
Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser			
225	230	235	240
cta gct gga aaa aga gag atg gct atc att act ttt aag aat ggt gca		768	
Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala			
245	250	255	
act ttt caa gta gaa gta cca ggt agt caa cat ata gat tca caa aaa		816	
Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys			
260	265	270	
aaa gcg att gaa agg atg aag gat acc ctg agg att gca tat ctt act		864	
Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr			
275	280	285	
gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa acg cct cat		912	
Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His			
290	295	300	
gcg att gcc gca att agt atg gca aat taa		942	
Ala Ile Ala Ala Ile Ser Met Ala Asn			
305	310		

<210> 16

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<400> 16

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
1 5 10 15Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
20 25 30Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
35 40 45Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
50 55 60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 65 70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 85 90 95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 100 105 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 130 135 140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 145 150 155 160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 165 170 175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
 180 185 190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly
 195 200 205

Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn
 210 215 220

Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser
 225 230 235 240

Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala
 245 250 255

Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys
 260 265 270

Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr
 275 280 285

Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His
 290 295 300

Ala Ile Ala Ala Ile Ser Met Ala Asn
 305 310

<210> 17
 <211> 1056
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct with

human and bacterial sequences

gtt tcc atc agc ttg tct gtt tca ttc cct gat gtt acg agc aat atg Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met 195 200 205 >	624
acc atc ttc tgt att ctg gaa act gac aag acg cggttta tct tca Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser 210 215 220	672
cct ttc tct ata gag ctt gag gac cct cag cct ccc cca gac cac gaa Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu 225 230 235 240	720
ttc ggc ggc tcc ggt ggt agc gcc aca cct caa aat att act gat ttg Phe Gly Gly Ser Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu 245 250 255	768
tgt gca gaa tac cac aac aca caa ata cat acg cta aat gat aag ata Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile 260 265 270	816
ttt tcg tat aca gaa tct cta gct gga aaa aga gag atg gct atc att Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile 275 280 285	864
act ttt aag aat ggt gca act ttt caa gta gaa gta cca ggt agt caa Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln 290 295 300	912
cat ata gat tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu 305 310 315 320	960
agg att gca tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp 325 330 335	1008
aat aat aaa acg cct cat gcg att gcc gca att agt atg gca aat taa Asn Asn Lys Thr Pro His Ala Ile Ala Ile Ser Met Ala Asn 340 345 350	1056

<210> 18

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<400> 18

Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
1 5 10 15Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
20 25 30

Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
 35 40 45
 Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
 50 55 60
 Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
 65 70 75 80
 Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
 85 90 95
 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
 100 105 110
 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
 115 120 125
 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn
 130 135 140
 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
 145 150 155 160
 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
 165 170 175
 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
 180 185 190
 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
 195 200 205
 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
 210 215 220
 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu
 225 230 235 240
 Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu
 245 250 255
 Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile
 260 265 270
 Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile
 275 280 285
 Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln
 290 295 300
 His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu
 305 310 315 320
 Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp
 325 330 335

Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
340 345 350

<210> 19
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 19
Ser Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala
1 5 10 15

Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln
20 25 30

<210> 20
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 20
Ala Gln Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln
1 5 10 15

Leu Lys Gln Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln
20 25 30

<210> 21
<211> 1095
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<220>
<221> CDS
<222> (1)..(1092)

<400> 21
atg gcc ata agt gga gtc cct gtg cta gga ttt ttc atc ata gct gtg 48
Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
1 5 10 15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile 20 25 30	96
atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met 35 40 45	144
ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys 50 55 60	192
gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu 65 70 75 80	240
gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ctg gaa Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu 85 90 95	288
atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro 100 105 110	336
gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn 115 120 125	384
gtc ctc atc tgt ttc atc gac aag ttc acc cca cca gtg gtc aat gtc Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val 130 135 140	432
acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr 145 150 155 160	480
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu 165 170 175	528
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His 180 185 190	576
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro 195 200 205	624
agc cct ctc cca gag act aca gag gaa ttc ggt ggt tcc ggt ggt tcc Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser 210 215 220	672
gcg cag ctg gaa tgg gaa ctg cag gcg ctg gaa aaa gaa aac gcg cag Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln 225 230 235 240	720

ctg gaa tgg gaa ctg cag gcg ctg gaa aaa gaa ctg gcg cag ggc ggc Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly 245 250 255	768
tcc ggt ggt agc gcc aca cct caa aat att act gat ttg tgt gca gaa Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu 260 265 270	816
tac cac aac aca caa ata cat acg cta aat gat aag ata ttt tcg tat Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr 275 280 285	864
aca gaa tct cta gct gga aaa aga gag atg gct atc att act ttt aag Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys 290 295 300	912
aat ggt gca act ttt caa gta gaa gta cca ggt agt caa cat ata gat Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp 305 310 315 320	960
tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg agg att gca Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala 325 330 335	1008
tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys 340 345 350	1056
acg cct cat gcg att gcc gca att agt atg gca aat taa Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn 355 360	1095

<210> 22
<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<400> 22 Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val 1 5 10 15
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile 20 25 30
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met 35 40 45
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys 50 55 60
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu 65 70 75 80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
 85 90 95
 Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110
 Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125
 Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
 130 135 140
 Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
 145 150 155 160
 Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
 165 170 175
 Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
 180 185 190
 Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
 195 200 205
 Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser
 210 215 220
 Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln
 225 230 235 240
 Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly
 245 250 255
 Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu
 260 265 270
 Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr
 275 280 285
 Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
 290 295 300
 Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
 305 310 315 320
 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
 325 330 335
 Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
 340 345 350
 Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 355 360

<210> 23
 <211> 861
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct with
 human and bacterial sequences

<220>
 <221> CDS
 <222> (1)..(855)

<400> 23

atg	gtg	tgt	ctg	aag	ttc	cct	gga	ggc	tcc	tgc	atg	gca	gct	ctg	aca	48
Met	Val	Cys	Leu	Lys	Phe	Pro	Gly	Gly	Ser	Cys	Met	Ala	Ala	Leu	Thr	
1															15	

gtg	aca	ctg	atg	gtg	ctg	agc	tcc	cca	ctg	gct	ttg	gct	ggg	gac	acc	96
Val	Thr	Leu	Met	Val	Leu	Ser	Ser	Pro	Leu	Ala	Leu	Ala	Gly	Asp	Thr	
20															30	

cga	cca	cgt	ttc	ttg	gag	cag	gtt	aaa	cat	gag	tgt	cat	ttc	ttc	aac	144
Arg	Pro	Arg	Phe	Leu	Glu	Gln	Val	Lys	His	Glu	Cys	His	Phe	Phe	Asn	
35															45	

ggg	acg	gag	cgg	gtg	cgg	ttc	ctg	gac	aga	tac	ttc	tat	cac	caa	gag	192
Gly	Thr	Glu	Arg	Val	Arg	Phe	Leu	Asp	Arg	Tyr	Phe	Tyr	His	Gln	Glu	
50															60	

gag	tac	gtg	cgc	ttc	gac	agc	gac	gtg	ggg	gag	tac	cgg	gcg	gtg	acg	240
Glu	Tyr	Val	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	
65															80	

gag	ctg	ggg	cgg	cct	gat	gcc	gag	tac	tgg	aac	agc	cag	aag	gac	ctc	288
Glu	Leu	Gly	Arg	Pro	Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Leu	
85															95	

ctg	gag	cag	aag	cgg	gcc	gcg	gtg	gac	acc	tac	tgc	aga	cac	aac	tac	336
Leu	Glu	Gln	Lys	Arg	Ala	Ala	Val	Asp	Thr	Tyr	Cys	Arg	His	Asn	Tyr	
100															110	

ggg	gtt	ggt	gag	agc	ttc	aca	gtg	cag	cgg	cga	gtc	tat	cct	gag	gtg	384
Gly	Val	Gly	Glu	Ser	Phe	Thr	Val	Gln	Arg	Arg	Val	Tyr	Pro	Glu	Val	
115															125	

act	gtg	tat	cct	gca	aag	acc	cag	ccc	ctg	cag	cac	cac	aac	ctc	ctg	432
Thr	Val	Tyr	Pro	Ala	Lys	Thr	Gln	Pro	Leu	Gln	His	His	Asn	Leu	Leu	
130															140	

gtc	tgc	tct	gtg	aat	ggt	ttc	tat	cca	ggc	agc	att	gaa	gtc	agg	tgg	480
Val	Cys	Ser	Val	Asn	Gly	Phe	Tyr	Pro	Gly	Ser	Ile	Glu	Val	Arg	Trp	
145															160	

ttc	cg	aa	gg	c	g	g	a	a	g	a	tt	gg	gt	gt	tcc	aca	gg	ct	528
Phe	Arg	Asn	Gly	Gln	Glu	Glu	Lys	Thr	Gly	Val	Val	Ser	Thr	Gly	Leu				
165																170	175		

atc cag aat gga gac tgg acc ttc cag acc ctg gtg atg ctg gaa aca Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr	576
180 185 190	
 gtt cct cgg agt gga gag gtt tac acc tgc caa gtg gag cac cca agc Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser	624
195 200 205	
 ctg acg agc cct ctc aca gtg gaa tgg aga gca cgg tct gaa tct gca Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala	672
210 215 220	
 cag agc aag ggc ggc tcc ggt ggt agc gcc cag ctg aag aag aaa ctc Gln Ser Lys Gly Ser Gly Ser Ala Gln Leu Lys Lys Lys Leu	720
225 230 235 240	
 cag gct ctg aaa aaa aag aat gcc cag ctc aag cag aag ctg cag gcc Gln Ala Leu Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala	768
245 250 255	
 ctg aag aaa aag ctg gct cag ggt tcc ggt ggt tcc gcg ggt ggt ggt Leu Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly	816
260 265 270	
 ttg aac gac atc ttc gaa gct cag aaa atc gaa tgg cac taataaa Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His	861
275 280 285	

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<210> 24
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct with
      human and bacterial sequences

<400> 24
Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr
 1           5                   10                      15

Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr
 20          25                   30

Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn
 35          40                   45

Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu
 50          55                   60

Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
 65          70                   75                      80

Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
 85          90                   95
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Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr
100 105 110

Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val
115 120 125

Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
130 135 140

Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
145 150 155 160

Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu
165 170 175

Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr
180 185 190

Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
195 200 205

Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
210 215 220

Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu
225 230 235 240

Gln Ala Leu Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala
245 250 255

Leu Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly
260 265 270

Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
275 280 285